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04/14/94

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/080,354BDATE: 04/13/94
TIME: 17:04:18

INPUT SET: S1962.raw

This Raw Listing contains only the General Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2

3 (1) General Information:

4
5 (i) APPLICANT: Breece, Tim
6 Hayenga, Kirk
7 Rinderknecht, Ernst
8 Vandlen, Richard
9 Yansura, Daniel

ENTERED

10
11 (iii) TITLE OF INVENTION: PROCESS FOR PRODUCING RELAXIN12
13 (iii) NUMBER OF SEQUENCES: 4014
15 (iv) CORRESPONDENCE ADDRESS:16 (A) ADDRESSEE: Mr. Walter H. Dreger
17 (B) STREET: 4 Embarcadero Center, Suite 3400
18 (C) CITY: San Francisco
19 (D) STATE: California
20 (E) COUNTRY: USA
21 (F) ZIP: 9411122
23 (v) COMPUTER READABLE FORM:24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.2528
29 (vi) CURRENT APPLICATION DATA:30 (A) APPLICATION NUMBER: US 08/080,354
31 (B) FILING DATE: 21-JUN-1993
32 (C) CLASSIFICATION:33
34 (viii) ATTORNEY/AGENT INFORMATION:35 (A) NAME: Dreger, Walter H.
36 (B) REGISTRATION NUMBER: 24,190
37 (C) REFERENCE/DOCKET NUMBER: A-58117/WHD38
39 (ix) TELECOMMUNICATION INFORMATION:40 (A) TELEPHONE: (415) 781-1989
41 (B) TELEFAX: (415) 398-324942
43 (2) INFORMATION FOR SEQ ID NO:1:44
45 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 11 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: peptide
53
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg
57 1 5 10
58
59
60 (2) INFORMATION FOR SEQ ID NO:2:
61
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 29 amino acids
64 (B) TYPE: amino acid
65 (C) STRANDEDNESS: single
66 (D) TOPOLOGY: linear
67
68 (ii) MOLECULE TYPE: peptide
69
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
71
72 Asp Ser Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val
73 1 5 10 15
74
75 Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser
76 20 25
77
78
79 (2) INFORMATION FOR SEQ ID NO:3:
80
81 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 13 amino acids
83 (B) TYPE: amino acid
84 (C) STRANDEDNESS: single
85 (D) TOPOLOGY: linear
86
87 (ii) MOLECULE TYPE: peptide
88
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
90
91 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg
92 1 5 10
93
94
95 (2) INFORMATION FOR SEQ ID NO:4:
96
97 (i) SEQUENCE CHARACTERISTICS:
98 (A) LENGTH: 24 amino acids
99 (B) TYPE: amino acid

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100 (C) STRANDEDNESS: single
101 (D) TOPOLOGY: linear
102
103 (ii) MOLECULE TYPE: peptide
104
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
106
107 Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr
108 1 5 10 15
109
110 Lys Arg Ser Leu Ala Arg Phe Cys
111 20
112
113
114 (2) INFORMATION FOR SEQ ID NO:5:
115
116 (i) SEQUENCE CHARACTERISTICS:
117 (A) LENGTH: 13 amino acids
118 (B) TYPE: amino acid
119 (C) STRANDEDNESS: single
120 (D) TOPOLOGY: linear
121
122 (ii) MOLECULE TYPE: peptide
123
124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
125
126 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg
127 1 5 10
128
129
130 (2) INFORMATION FOR SEQ ID NO:6:
131
132 (i) SEQUENCE CHARACTERISTICS:
133 (A) LENGTH: 13 amino acids
134 (B) TYPE: amino acid
135 (C) STRANDEDNESS: single
136 (D) TOPOLOGY: linear
137
138 (ii) MOLECULE TYPE: peptide
139
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
141
142 Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys
143 1 5 10
144
145
146 (2) INFORMATION FOR SEQ ID NO:7:
147
148 (i) SEQUENCE CHARACTERISTICS:
149 (A) LENGTH: 13 amino acids
150 (B) TYPE: amino acid
151 (C) STRANDEDNESS: single
152 (D) TOPOLOGY: linear

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153
154 (ii) MOLECULE TYPE: peptide
155
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
157
158 Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
159 1 5 10
160
161
162 (2) INFORMATION FOR SEQ ID NO:8:
163
164 (i) SEQUENCE CHARACTERISTICS:
165 (A) LENGTH: 13 amino acids
166 (B) TYPE: amino acid
167 (C) STRANDEDNESS: single
168 (D) TOPOLOGY: linear
169
170 (ii) MOLECULE TYPE: peptide
171
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
173
174 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
175 1 5 10
176
177
178 (2) INFORMATION FOR SEQ ID NO:9:
179
180 (i) SEQUENCE CHARACTERISTICS:
181 (A) LENGTH: 231 base pairs
182 (B) TYPE: nucleic acid
183 (C) STRANDEDNESS: single
184 (D) TOPOLOGY: linear
185
186 (ii) MOLECULE TYPE: cDNA
187
188 (ix) FEATURE:
189 (A) NAME/KEY: CDS
190 (B) LOCATION: 1..231
191
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
193
194 ATG AAA AAG AAT ATC GCA TTT CTT CTT AAA CGG GAC TCA TGG ATG GAG 48
195 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu
196 1 5 10 15
197
198 GAA GTT ATT AAA TTA TGC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC 96
199 Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala
200 20 25 30
201
202 ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC ACT GGT TAT GGT 144
203 Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly
204 35 40 45
205

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206	TCT CGA AAA AAG AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC	192
207	Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys	
208	50 55 60	

209		
210	CAT GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC	231
211	His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys	
212	65 70 75	

213

214

215 (2) INFORMATION FOR SEQ ID NO:10:

216

217 (i) SEQUENCE CHARACTERISTICS:
 218 (A) LENGTH: 593 base pairs
 219 (B) TYPE: nucleic acid
 220 (C) STRANDEDNESS: single
 221 (D) TOPOLOGY: linear

222

223 (ii) MOLECULE TYPE: cDNA

224

225 (ix) FEATURE:
 226 (A) NAME/KEY: CDS
 227 (B) LOCATION: 431..586

228

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

230

231	GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA	60
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232

233	GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA	120
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234

235	AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG	180
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236

237	GTTGATTGAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATT CCTGA	240
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238

239	CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA	300
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240

241	AAAAGTTAAT CTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT	360
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242

243	TGTTTTTATT TTTTAATGTA TTTGTACGCA AGTTCACGTA AAAAGGGTAT CTAGAGGTTG	420
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244

245	AGGTGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe	469
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246

247	1 5 10	
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248

249	GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA GAC TCA TGG ATG GAG GAA Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu	517
-----	--	-----

250

251	15 20 25	
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252

253	GTT ATT AAA TTA TGC GGC CGC GAA TTG GTA CGC GCG CAA ATA GCG ATA Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile	565
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254

255	30 35 40 45	
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256

257	TGC GGT ATG AGT ACA TGG AGT TGAAGAA 593	
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258	Cys Gly Met Ser Thr Trp Ser	
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SEQUENCE VERIFICATION REPORT
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Original Text